

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/537,143
Source: PCT
Date Processed by STIC: 3/2/06

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/537,143

DATE: 03/02/2006
TIME: 10:31:42

Input Set : E:\9632082999.txt
Output Set: N:\CRF4\03022006\J537143.raw

3 <110> APPLICANT: Franciso, Joseph
 4 McDonagh, Charlotte
 6 <120> TITLE OF INVENTION: MODIFIED L49-sFv EXHIBITING INCREASED STABILITY AND METHODS
 OF USE
 7 THEREOF
 9 <130> FILE REFERENCE: 9632-082-999
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/537,143
 C--> 12 <141> CURRENT FILING DATE: 2005-06-01
 14 <160> NUMBER OF SEQ ID NOS: 23
 15 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 753
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(753)
 27 <400> SEQUENCE: 1
 28 atg gag gtg cag ctt cag gag tca gga cct agc ctc gtg aaa cct tct 48
 29 Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser
 30 1 5 10 15
 31 cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt 96
 32 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser
 33 20 25 30
 34 ggt tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat 144
 35 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr
 36 35 40 45
 37 atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc 192
 38 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu
 39 50 55 60
 40 aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac 240
 41 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr
 42 65 70 75 80
 43 ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt 288
 44 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys
 45 85 90 95
 46 gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa 336
 47 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
 48 100 105 110
 49 gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa 384
 50 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys
 51 115 120 125
 52 ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa 432
 53 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln

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54	130	135	140	
55	act cca ctc tcc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct			480
56	Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser			
57	145	150	155	160
58	tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta			528
59	Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu			
60	165	170	175	
61	cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac			576
62	His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr			
63	180	185	190	
64	aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt			624
65	Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
66	195	200	205	
67	gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag			672
68	Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu			
69	210	215	220	
70	gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt cct ccg acg			720
71	Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr			
72	225	230	235	240
73	ttc ggt gga ggc acc aag ctg gaa atc aaa cg			753
74	Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg			
75	245	250		
77	<210> SEQ ID NO: 2			
78	<211> LENGTH: 251			
79	<212> TYPE: PRT			
80	<213> ORGANISM: Homo sapiens			
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83	Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser			
84	1	5	10	15
86	Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser			
87	20	25	30	
89	Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr			
90	35	40	45	
92	Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu			
93	50	55	60	
95	Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr			
96	65	70	75	80
98	Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys			
99	85	90	95	
101	Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln			
102	100	105	110	
104	Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys			
105	115	120	125	
107	Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln			
108	130	135	140	
110	Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser			
111	145	150	155	160
113	Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu			
114	165	170	175	

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116 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr		
117 180	185	190
119 Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser		
120 195	200	205
122 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu		
123 210	215	220
125 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr		
126 225	230	235
128 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg		240
129 245	250	
131 <210> SEQ ID NO: 3		
132 <211> LENGTH: 1839		
133 <212> TYPE: DNA		
134 <213> ORGANISM: Homo sapiens		
136 <220> FEATURE:		
137 <221> NAME/KEY: CDS		
138 <222> LOCATION: (1)...(1839)		
140 <400> SEQUENCE: 3		
141 atg gag gtg cag ctt cag gag tca gga cct agc ctc gtg aaa cct tct		48
142 Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser		
143 1 5 10 15		
144 cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt		96
145 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser		
146 20 25 30		
147 ggt tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat		144
148 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr		
149 35 40 45		
150 atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc		192
151 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu		
152 50 55 60		
153 aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac		240
154 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr		
155 65 70 75 80		
156 ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt		288
157 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys		
158 85 90 95		
159 gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa		336
160 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln		
161 100 105 110		
162 gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa		384
163 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys		
164 115 120 125		
165 ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa		432
166 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln		
167 130 135 140		
168 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct		480
169 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser		
170 145 150 155 160		
171 tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta		528

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172	Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu			
173	165	170	175	
174	cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac		576	
175	His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr			
176	180	185	190	
177	aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt		624	
178	Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
179	195	200	205	
180	gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag		672	
181	Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu			
182	210	215	220	
183	gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt cct ccg acg		720	
184	Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr			
185	225	230	235	240
186	tcc ggt gga ggc acc aag ctg gaa atc aaa cgg acg cca gtg tca gaa		768	
187	Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Pro Val Ser Glu			
188	245	250	255	
189	aaa cag ctg gcg gag gtg gtc gcg aat acg att acc ccg ctg atg aaa		816	
190	Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys			
191	260	265	270	
192	gcc cag tct gtt cca ggc atg gcg gtg gcc gtt att tat cag gga aaa		864	
193	Ala Gln Ser Val Pro Gly Met Ala Val Ala Ile Tyr Gln Gly Lys			
194	275	280	285	
195	ccg cac tat tac aca ttt ggc aag gcc gat atc gcg gcg aat aaa ccc		912	
196	Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro			
197	290	295	300	
198	gtt acg cct cag acc ctg ttc gag ctg ggt tct ata agt aaa acc ttc		960	
199	Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe			
200	305	310	315	320
201	acc ggc gtt tta ggt ggg gat gcc att gct cgc ggt gaa att tcg ctg		1008	
202	Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu			
203	325	330	335	
204	gac gat gcg gtg acc aga tac tgg cca cag ctg acg ggc aag cag tgg		1056	
205	Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp			
206	340	345	350	
207	cag ggt att cgt atg ctg gat ctc gcc acc tac acc gct ggc ggc ctg		1104	
208	Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu			
209	355	360	365	
210	ccg cta cag gta ccg gat gag gtc acg gat aac gcc tcc ctg ctg cgc		1152	
211	Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg			
212	370	375	380	
213	ttt tat caa aac tgg cag ccg cag tgg aag cct ggc aca acg cgt ctt		1200	
214	Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu			
215	385	390	395	400
216	tac gcc aac gcc agc atc ggt ctt ttt ggt gcg ctg gcg gtc aaa cct		1248	
217	Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro			
218	405	410	415	
219	tct ggc atg ccc tat gag cag gcc atg acg acg cgg gtc ctt aag ccg		1296	
220	Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro			

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221	420	425	430	
222	ctc aag ctg gac cat acc tgg att aac gtg ccg aaa gca gaa gag gcg			1344
223	Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala			
224	435	440	445	
225	cat tac gcc tgg ggc tat cgt gac ggt aaa gca gtc cgc gtt tcg ccg			1392
226	His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro			
227	450	455	460	
228	ggt atg ctg gat gca caa gcc tat ggc gtc aaa acc aac gtg cag gat			1440
229	Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp			
230	465	470	475	480
231	atg gcg aac tgg gtc atg gca aac atg gca ccg gag aac gtt gct gat			1488
232	Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp			
233	485	490	495	
234	gcc tca ctt aag cag ggc atc gca ctg gca cag tcg cgc tac tgg cgt			1536
235	Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg			
236	500	505	510	
237	atc ggg tca atg tat cag ggt ctg ggc tgg gag atg ctc aac tgg ccc			1584
238	Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro			
239	515	520	525	
240	gtg gag gcc aac acg gtg gtc gag acg agt ttt ggt aat gta gca ctg			1632
241	Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu			
242	530	535	540	
243	gca ccg ttg ccc gtg gca gaa gtg aat cca ccg gct ccc ccg gtc aaa			1680
244	Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys			
245	545	550	555	560
246	gca tcc tgg gtc cat aaa acg ggc tct act ggc ggg ttt ggc agc tac			1728
247	Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr			
248	565	570	575	
249	gtg gcc ttt att cct gaa aag cag atc ggt att gtg atg ctc gcg aat			1776
250	Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn			
251	580	585	590	
252	aca agc tat ccg aac ccg gca ccg gtt gag gca tac cat atc ctc			1824
253	Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu			
254	595	600	605	
255	gag gca cta cag tag			1839
256	Glu Ala Leu Gln			
257	610			
259	<210> SEQ ID NO: 4			
260	<211> LENGTH: 612			
261	<212> TYPE: PRT			
262	<213> ORGANISM: Homo sapiens			
264	<400> SEQUENCE: 4			
265	Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser			
266	1	5	10	15
268	Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser			
269	20	25	30	
271	Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr			
272	35	40	45	
274	Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu			

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/02/2006
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Input Set : E:\9632082999.txt
Output Set: N:\CRF4\03022006\J537143.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23

VERIFICATION SUMMARY

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DATE: 03/02/2006

TIME: 10:31:43

Input Set : E:\9632082999.txt

Output Set: N:\CRF4\03022006\J537143.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date